

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: The Regents of the University of California

(ii) TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS

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(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

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(A) ADDRESSEE: Robbins, Berliner & Carson

(B) STREET: 201 N. Figueroa Street, 5th Floor

(C) CITY: Los Angeles

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 90012-2628

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

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(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

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(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Berliner, Robert

(B) REGISTRATION NUMBER: 20,121

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(C) REFERENCE/DOCKET NUMBER: 5555-291

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 310-977-1001

(B) TELEFAX: 310-977-1003

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(C) TELEX:

005270" C/4552960

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 40..1161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20

GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT 54
 Met Leu Ser Thr Ser
 1 5

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CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC 102
 Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr
 10 15 20

30

ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG 150
 Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val
 25 30 35

35

AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC 198
 Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
 40 45 50

40

ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC 246
 Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn
 55 60 65

TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC 294
 Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala
 70 75 80 85

45

ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT 342
 Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser
 90 95 100

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	GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA	390
	Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr	
	105 110 115	
5	GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC	438
	Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu	
	120 125 130	
10	CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA	486
	Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu	
	135 140 145	
15	AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG	534
	Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp	
	150 155 160 165	
20	TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC	582
	Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys	
	170 175 180	
25	CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA	630
	Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly	
	185 190 195	
30	TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG	678
	Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu	
	200 205 210	
35	CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG	726
	Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu	
	215 220 225	
40	CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC	774
	Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile	
	230 235 240 245	
45	TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT	822
	Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile	
	250 255 260	
50	GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT	870
	Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys	
	265 270 275	
55	GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT	918
	Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu	
	280 285 290	

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	GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG	966
	Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly	
	295 300 305	
5	GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC	1014
	Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala	
	310 315 320 325	
10	CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG	1062
	Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys	
	330 335 340	
15	AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA	1110
	Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly	
	345 350 355	
20	AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA	1158
	Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly	
	360 365 370	
	GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC	1211
	Ala	
25	ACAGATGTGT GATTCACAGT GTGAATCTTG GTGTCTACGT TACCAGGCAG GAAGGCTGAG	1271
	AGGAGAGAGA CTCCAGCTGG GTTGAAAAAC AGTATTTTCC AAACCTACCTT CCAGTTCCTC	1331
30	ATTTTGAAT ACAGGCATAG AGTTCAGACT TTTTITAAAT AGTAAAAATA AAATTAAAGC	1391
	TGAAAACGTC AACTTGTAAG TGTGGTAAAG AGTTAGTTTG AGTTGCTATC ATGTCAAACG	1451
	TGAAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG	1511
35	GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA	1571
	GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT	1631
40	TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTC TCTCAGGCTT	1691
	GCTGCCAAAA GCCTTTTGTG TTTTGTITTG TATCATTATG AAGTCATGCG TTTAATCACA	1751
	TTCGAGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTGCCA	1811
45	GTGGGAACCTC CTAAATCAAA TTGGCTTCTA ATCAAAGCTT TTAACCCTA TTGGTAAAGA	1871
	ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT	1931
	AAGAATGTTT TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC	1991

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51.

TTCTAGAACC AGGCAACTTG GGAAGTAGAC TCCCAAGCTG GACTATGGCT CTACTTTCAG 2051
 GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA 2111
 5 TATATTTGTA TGATCCTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA 2171
 TACTGTTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATACTAT GTTGATAAAA 2231
 G 2232
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
 1 5 10 15
 25 Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
 20 25 30
 30 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
 35 40 45
 Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
 50 55 60
 35 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
 65 70 75 80
 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
 85 90 95
 40 Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
 100 105 110
 45 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
 115 120 125
 Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 130 135 140

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52.

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
145 150 155 160

5 Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
180 185 190

10 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
195 200 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
210 215 220

15 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
225 230 235 240

20 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
260 265 270

25 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
275 280 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
290 295 300

30 Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
305 310 315 320

35 Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
325 330 335

Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
340 345 350

40 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
355 360 365

Gln Asp Lys Glu Gly Ala
370

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1979 base pairs

005573.072500

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 81..1160

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT	60
	TTCCCCAGTA CATCCACAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC	110
	Met Leu Ser Thr Ser Arg Ser Arg Phe Ile	
	1 5 10	
25	AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT	158
	Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr	
	15 20 25	
30	GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC	206
	Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala	
	30 35 40	
35	CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG	254
	Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val	
	45 50 55	
40	GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG	302
	Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys	
	60 65 70	
	TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT	350
	Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu	
	75 80 85 90	
45	TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG	398
	Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp	
	95 100 105	

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	GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile 110 115 120	446
5	GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg 125 130 135	494
10	TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val 140 145 150	542
15	ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val Ala Val Phe 155 160 165 170	590
20	GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC CAG AAA GAA GAT TCT Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser 175 180 185	638
	GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA TGG AAT AAT TTC CAC Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly Trp Asn Asn Phe His 190 195 200	686
25	ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG CCG CTG CTC ATC ATG Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu Pro Leu Leu Ile Met 205 210 215	734
30	GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG CTT CGG TGT CGA AAC Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn 220 225 230	782
35	GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC TTC ACC ATC ATG ATT Glu Lys Lys Arg His Arg Ala Val Arg Val Ile Phe Thr Ile Met Ile 235 240 245 250	830
40	GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT GTC ATT CTC CTG AAC Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn 255 260 265	878
	ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT GAA AGC ACC AGT CAA Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln 270 275 280	926
45	CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT GGG ATG ACT CAC TGC Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu Gly Met Thr His Cys 285 290 295	974

	TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG GAG AAG TTC AGA AGG	1022
	Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg	
	300 305 310	
5	TAT CTC TCG GTG TTC TTC CGA AAG CAC ATC ACC AAG CGC TTC TGC AAA	1070
	Tyr Leu Ser Val Phe Phe Arg Lys His Ile Thr Lys Arg Phe Cys Lys	
	315 320 325 330	
10	CAA TGT CCA GTT TTC TAC AGG GAG ACA GTG GAT GGA GTG ACT TCA ACA	1118
	Gln Cys Pro Val Phe Tyr Arg Glu Thr Val Asp Gly Val Thr Ser Thr	
	335 340 345	
15	AAC ACG CCT TCC ACT GGG GAG CAG GAA GTC TCG GCT GGT TTA	1160
	Asn Thr Pro Ser Thr Gly Glu Gln Glu Val Ser Ala Gly Leu	
	350 355 360	
20	TAAACGAGG AGCAGTTTGA TTGTTGTTTA TAAAGGGAGA TAACAATCTG TATATAACAA	1220
	CAAACCTTCAA GGGTTTGTG AACAAAGAA ACCTGTAAAG CAGGTGCCCA GGAACCTCAG	1280
	GGCTGTGTGT ACTAATACAG ACTATGTCAC CCAATGCATA TCCAACATGT GCTCAGGGAA	1340
	TAATCCAGAA AAACGTGGG TAGAGACTTT GACTCTCCAG AAAGCTCATC TCAGCTCCTG	1400
25	AAAAATGCCT CATTACCTTG TGCTAATCCT CTTTTCTAG TCTTCATAAT TTCTTCACTC	1460
	AATCTCTGAT TCTGTCAATG TCTTGAAATC AAGGGCCAGC TGGAGGTGAA GAAGAGAATG	1520
30	TGACAGGCAC AGATGAATGG GAGTGAGGGA TAGTGGGGTC AGGGCTGAGA GGAGAAGGAG	1580
	GGAGACATGA GCATGGCTGA GCCTGGACAA AGACAAAGGT GAGCAAAGGG CTCACGCATT	1640
	CAGCCAGGAG ATGATACTGG TCCTTAGCCC CATCTGCCAC GTGTATTTAA CCTTGAAGGG	1700
35	TTCAACAGGT CAGGGAGAGT TTGGGAACTG CAATAACCTG GGAGTTTTGG TGGAGTCCGA	1760
	TGATTCTCTT TTGCATAAGT GCATGACATA TTTTGTCTT ATTACAGTTT ATCTATGGCA	1820
40	CCCATGCACC TTACATTGA AATCTATGAA ATATCATGCT CCATTGTTCA GATGCTTCTT	1880
	AGGCCACATC CCCCTGTCTA AAAATTCAGA AAATTTTGT TTATAAAAGA TGCATTATCT	1940
45	ATGATATGCT AATATATGTA TATGCAATAT AAAATTTAG	1979

00520E2596

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
1 5 10 15

15

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
20 25 30

His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
35 40 45

20

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
50 55 60

25

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
65 70 75 80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
85 90 95

30

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
100 105 110

Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
115 120 125

35

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
130 135 140

40

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
165 170 175

45

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
180 185 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
195 200 205

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57.

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
210 215 220

5 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
245 250 255

10 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
260 265 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
275 280 285

15 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
290 295 300

20 Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Leu Ser Val Phe Phe
305 310 315 320

Arg Lys His Ile Thr Lys Arg Phe Cys Lys Gln Cys Pro Val Phe Tyr
325 330 335

25 Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly
340 345 350

Glu Gln Glu Val Ser Ala Gly Leu
355 360

30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
1 5 10 15

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58.

	Asp	Tyr	Gly	Asp	Ala	Thr	Pro	Cys	Gln	Lys	Val	Asn	Glu	Arg	Ala	Phe	
				20					25					30			
5	Gly	Ala	Gln	Leu	Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Val	Ile	Gly	
			35					40					45				
	Leu	Val	Gly	Asn	Ile	Leu	Val	Val	Leu	Val	Leu	Val	Gln	Tyr	Lys	Arg	
			50				55					60					
10	Leu	Lys	Asn	Met	Thr	Ser	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	
		65					70				75				80		
	Leu	Leu	Phe	Leu	Phe	Thr	Leu	Pro	Phe	Trp	Ile	Asp	Tyr	Lys	Leu	Lys	
					85					90					95		
15	Asp	Asp	Trp	Val	Phe	Gly	Asp	Ala	Met	Cys	Lys	Ile	Leu	Ser	Gly	Phe	
				100					105						110		
	Tyr	Tyr	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	
20				115					120					125			
	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala	
			130					135					140				
25	Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Ile	Ile	Trp	Ala	Leu	
		145					150				155				160		
	Ala	Ile	Leu	Ala	Ser	Met	Pro	Gly	Leu	Tyr	Phe	Ser	Lys	Thr	Gln	Trp	
					165					170					175		
30	Glu	Phe	Thr	His	His	Thr	Cys	Ser	Leu	His	Phe	Pro	His	Glu	Ser	Leu	
				180						185					190		
	Arg	Glu	Trp	Lys	Leu	Phe	Gln	Ala	Leu	Lys	Leu	Asn	Leu	Phe	Gly	Leu	
35			195						200					205			
	Val	Leu	Pro	Leu	Leu	Val	Met	Ile	Ile	Cys	Tyr	Thr	Gly	Ile	Ile	Lys	
			210					215					220				
40	Ile	Leu	Leu	Arg	Arg	Pro	Asn	Glu	Lys	Lys	Ser	Lys	Ala	Val	Arg	Leu	
		225					230					235			240		
	Ile	Phe	Val	Ile	Met	Ile	Ile	Phe	Phe	Leu	Phe	Trp	Thr	Pro	Tyr	Asn	
				245					250						255		
45	Leu	Thr	Ile	Leu	Ile	Ser	Val	Phe	Gln	Asp	Phe	Leu	Phe	Thr	His	Glu	
				260					265					270			

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59.

Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
275 280 285

5 Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
305 310 315 320

10 Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
325 330 335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser
340 345 350

15 Ala Gly Phe
355

20 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
1 5 10 15

Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
20 25 30

Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Tyr Ile Tyr Ser Ile Ile
35 40 45

Phe Leu Tyr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
50 55 60

Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
65 70 75 80

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Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val
 85 90 95

5 Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val
 100 105 110

His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala
 115 120 125

10 Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser
 130 135 140

Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val
 15 145 150 155 160

Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn
 165 170 175

Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn
 20 180 185 190

Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
 195 200 205

25 Ile Leu Pro Gly Ile Val Ile Leu Phe Cys Tyr Cys Ile Ile Ile Ser
 210 215 220

Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Tyr
 30 225 230 235 240

Tyr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
 245 250 255

35 Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln
 260 265 270

Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
 275 280 285

40 Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
 290 295 300

Leu Gly Ala Lys Phe Lys Tyr Ser Ala Gln His Ala Leu Thr Ser Val
 45 305 310 315 320

Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
 325 330 335

005240" 2552960

His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
 340 345 350

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe Asp Asp Leu Asn
 1 5 10 15

Phe Thr Gly Met Pro Pro Ala Asp Glu Asp Tyr Ser Pro Cys Met Leu
 20 25 30

Glu Thr Glu Thr Leu Asn Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu
 35 40 45

Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met Leu Val Ile
 50 55 60

Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr Leu Leu Asn
 65 70 75 80

Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro Ile Trp Ala
 85 90 95

Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu Cys Lys Val
 100 105 110

Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu Leu Leu
 115 120 125

Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His Ala Thr Arg
 130 135 140

005270" 072500

62.

Thr Leu Thr Gln Lys Arg His Leu Val Lys Phe Val Cys Leu Gly Cys
145 150 155 160

5

Trp Gly Leu Ser Met Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg Gln
165 170 175

Ala Tyr His Pro Asn Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly
180 185 190

10

Asn Asp Thr Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His Thr
195 200 205

Phe Gly Phe Ile Val Pro Leu Phe Val Met Leu Phe Cys Tyr Gly Phe
210 215 220

15

Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys His Arg Ala
225 230 235 240

20

Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp Leu
245 250 255

Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr Gln Val
260 265 270

25

Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg Ala Leu Asp
275 280 285

Ala Thr Glu Ile Leu Gly Phe Leu His Ser Cys Leu Asn Pro Ile Ile
290 295 300

30

Tyr Ala Phe Ile Gly Gln Asn Phe Arg His Gly Phe Leu Lys Ile Leu
305 310 315 320

35

Ala Met His Gly Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val
325 330 335

Thr Ser Tyr Thr Ser Ser Ser Val Asn Val Ser Ser Asn Leu
340 345 350

40

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

45

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Met Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser
 1 5 10 15
 Asn Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala
 20 25 30
 10 Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile
 35 40 45
 Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val
 50 55 60
 15 Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val
 65 70 75 80
 Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu
 85 90 95
 20 Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe
 100 105 110
 25 Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly
 115 120 125
 Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val
 130 135 140
 30 His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile
 145 150 155 160
 35 Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu
 165 170 175
 Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr
 180 185 190
 40 Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile
 195 200 205
 Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe
 210 215 220
 45 Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln
 225 230 235 240

005270" E252950

64.

Lys His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu
245 250 255

5 Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met
260 265 270

Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn His Ile Asp
275 280 285

10 Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu
290 295 300

Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu
305 310 315 320

15 Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro
325 330 335

20 Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser
340 345 350

Thr Thr Leu
355

25 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (synthetic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCTCGAGAC CTRKCMDTKK CYGACCT

27

45 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid

005220" E255260

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGAATTCTG GACRATGGCC AGGTAVCKGT C

31

15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Leu Ala Ile Ser Asp Leu
1 5

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Arg Tyr Leu Ala Ile Val
1 5

45

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

005270 E 252960

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10

Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val
 1 5 10 15

His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val
 20 25 30

15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val
 1 5 10 15

30

His Ala Val Phe Ala Leu Arg Ala Arg Thr Val Thr Phe Gly Val
 20 25 30

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